

## Cytological notes in Rutaceae. 1: *Boronia tenuis*

Helen M. Stace<sup>1</sup> & S. J. Patrick<sup>2</sup>

<sup>1</sup>Botany Department, University of Western Australia, Nedlands, Western Australia 6009

<sup>2</sup>Western Australian Herbarium, Department of Conservation and Land Management,  
PO Box 104, Como, Western Australia 6152

### Abstract

Helen M. Stace & Patrick, S.J. Cytological notes in Rutaceae. 1: *Boronia tenuis*. Nuytsia 9(1): 131-133 (1993). A new chromosome number determination for *Boronia tenuis* ( $n=16$ ) corrects a prior report and has implications for the cytotaxonomy of *Boronia* in Western Australia.

### Introduction

*Boronia* Sm. (c. 100 spp.) is the largest genus of the Australasian tribe Boronieae (Rutaceae) and more than 45 species are Western Australian (Green 1985). The genus shows considerable cytoevolution through dysploidy from  $x=18$  to  $n=7$  (Smith-White 1954, Stace & Armstrong 1992). *Boronia* is of key interest in the cytotaxonomy of the Boronieae and family Rutaceae, as Smith-White (1954) utilised the available cytological data to argue that the genus, tribe and family had evolved from a base number of  $x=9$  with most higher numbers having evolved from ancient polyploid ancestors (paleopolyploidy). This view was followed by Weston *et al.* (1984) in their cladistic analysis of *Boronia*, but their cladogram incorporating chromosome number information was reinterpreted by Stace *et al.* (1993) to show that *Boronia*, Boronieae and Rutaceae had evolved from a probable diploid base of  $x=18$ .

One of the key species supporting the possibility that *Boronia* had evolved on  $x=9$  is *B. tenuis* Benth. This relatively rare species is known from several populations along the Darling Scarp, Western Australia (Patrick & Hopper 1981, Marchant *et al.* 1987) and at Cape Naturaliste some 150 km south-west of the Scarp populations. It was reported as  $n=9$  by Smith-White (1954) although all cytologically known related species in section *Cyanothamnus* (Bentham 1863, Weston *et al.* 1984) are  $x=18$  ( $n=18, 36$ ). This note re-examines Smith-White's report in verified collections of *B. tenuis* from two localities east and south-east of Perth.

### Methods

Young floral buds of *B. tenuis* plants from Bickley and North Dandalup were fixed in Bradley's fluid, and anther squashes stained in Snow's alcoholic carmine were examined for pollen mother cell (p.m.c.) meiosis. Vouchers (S.J. Patrick 1049, 1050) are housed at the Western Australian Herbarium (PERTH).

## Results

Meiotic metaphase I and II cells clearly indicate that *B. tenuis* is  $n=16$  from both populations (Figure 1). Meiosis is normal with no indications of multivalent formation. The two locations are about 60 km apart and sample much of the species' known distribution on the Darling Scarp.



Figure 1. Meiosis in *B. tenuis*,  $n=16$ ; metaphase I, polar view, showing sixteen bivalents. Bickley, Western Australia.

## Discussion

*B. tenuis* is a small diffuse perennial plant and apparently rather advanced both morphologically and cytologically within section *Cyanothamnus* where six other species are presently reported as  $x=18$ . This is the first report of  $n=16$  in a species of this section, but it is consistent with dysploid cytoevolution from  $x=18$ . In certain key characters *B. tenuis* groups with four other WA species *B. busselliana* F. Muell., *B. defoliata* F. Muell., *B. fabianooides* (Diels) P. G. Wilson and *B. subsessilis* Benth. (Weston *et al.* 1984) and it remains to be seen whether  $n=16$  is typical of this and any other subgroupings of *Boronia-Cyanothamnus* species. Other reports of  $n=16$  occur in eastern Australian species of section *Valvatae* (Smith-White 1954, Weston *et al.* 1984), where, presumably, it has evolved independently.

Smith-White's voucher of '*B. tenuis*' from Albany has not been found, but probably the species determination was incorrect as *B. tenuis* Benth. is not known to occur in that district (P.G. Wilson, pers. comm.). It is clear that  $n=9$  is neither definitive nor typical for *B. tenuis* Benth. Our new determination discounts the paleopolyploid model but further affirms the value of diploid chromosome number information in the taxonomy and evolution of *Boronia* (Smith-White 1954). Two-thirds of the genus are cytologically unknown but offer an intriguing area for future cytoevolutionary and ecological genetics research.

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